amdt D

SEQUENCE LISTING

<110> Oklahoma Medical Research Foundation
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Rufer, Andreas Walter

SubD

<120> Method for Selecting Recombinase Variants with Altered Specificity

<130> OMRF 178

<140> 09/544,045
<141> 2000-04-06

<150> 60/127,977
<151> 1999-04-06

<160> 68

<170> PatentIn version 3.1

<210> 1
<211> 343
<212> PRT
<213> Artificial Sequence

<220>
<223> Cre

<400> 1

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Asp Ala Thr Ser Asp Glu Val Arg Lys Asn Leu Met Asp Met Phe Arg
20 25 30

Asp Arg Gln Ala Phe Ser Glu His Thr Trp Lys Met Leu Leu Ser Val
35 40 45

Cys Arg Ser Trp Ala Ala Trp Cys Lys Leu Asn Asn Arg Lys Trp Phe
50 55 60

Pro Ala Glu Pro Glu Asp Val Arg Asp Tyr Leu Leu Tyr Leu Gln Ala

65 70 75 80

Arg Gly Leu Ala Val Lys Thr Ile Gln Gln His Leu Gly Gln Leu Asn
85 90 95

Met Leu His Arg Arg Ser Gly Leu Pro Arg Pro Ser Asp Ser Asn Ala
100 105 110

Val Ser Leu Val Met Arg Arg Ile Arg Lys Glu Asn Val Asp Ala Gly
115 120 125

Glu Arg Ala Lys Gln Ala Leu Ala Phe Glu Arg Thr Asp Phe Asp Gln
130 135 140

Val Arg Ser Leu Met Glu Asn Ser Asp Arg Cys Gln Asp Ile Arg Asn
145 150 155 160

Leu Ala Phe Leu Gly Ile Ala Tyr Asn Thr Leu Leu Arg Ile Ala Glu
165 170 175

Ile Ala Arg Ile Arg Val Lys Asp Ile Ser Arg Thr Asp Gly Gly Arg
180 185 190

Met Leu Ile His Ile Gly Arg Thr Lys Thr Leu Val Ser Thr Ala Gly
195 200 205

Val Glu Lys Ala Leu Ser Leu Gly Val Thr Lys Leu Val Glu Arg Trp
210 215 220

Ile Ser Val Ser Gly Val Ala Asp Asp Pro Asn Asn Tyr Leu Phe Cys
225 230 235 240

Arg Val Arg Lys Asn Gly Val Ala Ala Pro Ser Ala Thr Ser Gln Leu
245 250 255

Ser Thr Arg Ala Leu Glu Gly Ile Phe Glu Ala Thr His Arg Leu Ile

260 265 270

Tyr Gly Ala Lys Asp Asp Ser Gly Gln Arg Tyr Leu Ala Trp Ser Gly
275 280 285

His Ser Ala Arg Val Gly Ala Ala Arg Asp Met Ala Arg Ala Gly Val
290 295 300

Ser Ile Pro Glu Ile Met Gln Ala Gly Gly Trp Thr Asn Val Asn Ile
305 310 315 320

Val Met Asn Tyr Ile Arg Asn Leu Asp Ser Glu Thr Gly Ala Met Val
325 330 335

Arg Leu Leu Glu Asp Gly Asp
340

<210> 2
<211> 13
<212> DNA
<213> artificial sequence

<220>
<223> Inverted repeat sequence

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<222> (1)..(3)
<223> N at positions 1-3 can be A, T, G, or C.

<220>
<221> misc_feature
<222> (6)..(7)
<223> N at positions 6 and 7 can be A, T, G, or C.

<400> 2
nnnacnncgt ata
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<210> 3
<211> 34
<212> DNA
<213> artificial sequence

<220>
<223> variant lox sites

<220>
<221> misc_feature
<222> (1)..(3)
<223> N at postitions 1-3 can be A, G, C, or T

<220>
<221> misc_feature
<222> (6)..(7)
<223> N at positions 6 and 7 can be A, T, G, C,

<220>
<221> misc_feature
<222> (14)..(21)
<223> N at positions 14-21 can A, G, T, or C

<220>
<221> misc_feature
<222> (28)..(29)
<223> N at postions 28 and 29 can be A, T, G, or C

<220>
<221> misc_feature
<222> (32)..(34)
<223> N at postiions 32-34 can be A, T, G, or C

<400> 3
nnnacnncgt atannnnnnn ntatacgnng tnnn
34

<210> 4
<211> 33
<212> DNA
<213> artificial sequence

<220>
<223> variant lox sites

<400> 4
gatacaacgt atataccttt ctatacgttg tat
33

<210> 5
<211> 34
<212> DNA
<213> artificial sequence

<220>
<223> Specific and non-specific sequences for Cre recombinase

<220>
<221> misc_feature
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<223> N at postions 1-3 can be A, T, G, or C

<220>
<221> misc_feature
<222> (14)..(21)
<223> N at positions 14-21 can be A, T, C, or G

<220>
<221> misc_feature
<222> (32)..(34)
<223> N at positions 32-34 can be A, T, G, or C

<400> 5
nnnacttcgt atannnnnnn ntatacgaag tnnn
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<210> 6
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> oligonucleotide

<400> 6

Ala Thr Arg Val Asx Tyr Gly Cys
1 5

<210> 7
<211> 34
<212> DNA
<213> artificial sequence

<220>
<223> primer

<400> 7
ataacttcgt ataatgtatg ctatacgaag ttat
34

<210> 8
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<212> DNA
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<220>
<223> primer

<400> 8
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<210> 9
<211> 31
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<220>
<223> primer

<400> 9
atatataagc ttatcattta cgcgttaatg g
31

<210> 10
<211> 33
<212> DNA
<213> artificial sequence

<220>
<223> primer

<400> 10
ataagcggcc gctgagcttg gctgttttgg cgg
33

<210> 11
<211> 36
<212> DNA
<213> artificial sequence

<220>
<223> primer

<400> 11
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36

<210> 12
<211> 30
<212> DNA
<213> artificial sequence

<220>
<223> primer

<400> 12
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<210> 13
<211> 36
<212> DNA
<213> artificial sequence

<220>
<223> primer

<400> 13
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36

<210> 14
<211> 20
<212> DNA
<213> artificial sequence

<220>
<223> primer

<400> 14
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<210> 15
<211> 20
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<213> artificial sequence

<220>
<223> primer

<400> 15
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<210> 16
<211> 20
<212> DNA
<213> artificial sequence

<220>
<223> primer

<400> 16
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20

<210> 17
<211> 18
<212> DNA
<213> artificial sequence

<220>
<223> primer

<400> 17

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<210> 18
<211> 21
<212> DNA
<213> artificial sequence

<220>
<223> primer

<400> 18
tctgcgttct gatttaatct g
21

<210> 19
<211> 18
<212> DNA
<213> artificial sequence

<220>
<223> primer

<400> 19
ccaggccagg tatctctg
18

<210> 20
<211> 22
<212> DNA
<213> artificial sequence

<220>
<223> primer

<400> 20
gtacgtgaga tatctttaac cc
22

<210> 21
<211> 22
<212> DNA
<213> artificial sequence

<220>
<223> primer

<400> 21
ttgctggata gtttttactg cc
22

<210> 22
<211> 45
<212> DNA
<213> artificial sequence

<220>
<223> primer

<400> 22
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45

<210> 23
<211> 45
<212> DNA
<213> artificial sequence

<220>
<223> primer

<400> 23
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45

<210> 24
<211> 45
<212> DNA
<213> artificial sequence

<220>
<223> primer

<400> 24
gctatcaact cgcgccctgg cagggatttt tgaagcaact catcg
45

<210> 25

<211> 45
<212> DNA
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<220>
<223> primer

<400> 25
gagttgcttc aaaaatccct gccagggcgc gagttgatag ctggc
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<210> 26
<211> 45
<212> DNA
<213> artificial sequence

<220>
<223> primer

<220>
<221> misc_feature
<222> (17)..(25)
<223> N at positions 17-25 can be A, T, G, or C

<400> 26
gctatcaact cgcgccnnnn nnnnnatttt tgaagcaact catcg
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<210> 27
<211> 45
<212> DNA
<213> artificial sequence

<220>
<223> primer

<220>
<221> misc_feature
<222> (17)..(25)
<223> N at positions 17-25 can be A, T, G, or C

<400> 27
gagttgcttc aaaaatnnnn nnnnnggcgc gagttgatag ctggc
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<210> 28
<211> 1172
<212> DNA
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<220>
<223> wtCre

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120

ggttcgcaag aacctgatgg acatgttcag ggatcgccag gcgttttctg agcatacctg
180

gaaaatgctt ctgtccgttt gccggtcgtg ggcggcatgg tgcaagttga ataaccggaa
240

atggtttccc gcagaacctg aagatgttcg cgattatctt ctatatcttc aggcgcgcgg
300

tctggcagta aaaactatcc agcaacattt gggccagcta aacatgcttc atcgtcggtc
360

cgggctgcca cgaccaagtg acagcaatgc tgtttcactg gttatgcggc ggatccgaaa
420

agaaaacgtt gatgccggtg aacgtgcaaa acaggctcta gcgttcgaac gcactgattt
480

cgaccaggtt cgttcactca tggaaaatag cgatcgctgc caggatatac gtaatctggc
540

atttctgggg attgcttata acaccctgtt acgtatagcc gaaattgcca ggatcagggt
600

taaagatatc tcacgtactg acggtgggag aatgttaatc catattggca gaacgaaaac
660

gctggttagc accgcaggtg tagagaaggc acttagcctg ggggtaacta aactggtcga
720

gcgatggatt tccgtctctg gtgtagctga tgatccgaat aactacctgt tttgccgggt

780

cagaaaaaat ggtgttgccg cgccatctgc caccagccag ctatcaactc gcgccctgga
840

agggattttt gaagcaactc atcgattgat ttacggcgct aaggatgact ctggtcagag
900

atacctggcc tggtctggac acagtgcccg tgtcggagcc gcgcgagata tggcccgcgc
960

tggagtttca ataccggaga tcatgcaagc tggtggctgg accaatgtaa atattgtcat
1020

gaactatatc cgtaacctgg atagtgaaac aggggcaatg gtgcgcctgc tggaagatgg
1080

cgattagcca ttaacgcgta aatgataagc ttggctgttt tggcggatga gagaagattt
1140

tcagcctgat acagattaaa tcagaacgca ga
1172

<210> 29
<211> 1172
<212> DNA
<213> artificial sequence

<220>
<223> mxoxox1

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60

caatttactg accgtacacc aaaatttgcc tgcattacct gtcgatgcaa cgagtgatga
120

ggttcgcaag aacctgatgg ccatgttcag ggatcgccag gcgttttctg agcatacctg
180

gaaaatgctt ctgtccgttt gccggtcgtg ggcggcatgg tgcaagttga ataaccggaa
240

atggtttccc gcagaacctg aagatgttcg cgattatctt ctatatcttc aggcgcgcgg
300

tctggcagta aaaactatcc agcaacattt gggccagcta aacatgcttc atcgtcggtc
360

cgggctgcca cgaccaagtg acagcaatgc tgtttcactg gttatgcggc ggatccgaaa
420

agaaaacgtt gatgccggtg aacgtgcaaa acaggctcta gcgttcgaac gcactgattt
480

cgaccaggtt cgttcactca tggaaaatag cgatcgctgc caggatatac gtaatctggc
540

atttctgggg attgcttata acaccctgtt acgtatagcc gaaattgcca ggatcagggt
600

taaagatatc tcacgtacta acggtgggag aatgttaatc catattggca gaacgaaaac
660

gctggttagc accgcaggtg tagagaaggc acttagtctg ggggtaacta aactggtcga
720

gcgatggatt tccatctctg gtgtagctga tgatccgaat aactacctgt tttgccgggt
780

cagaaaaaat ggtgttgccg cgccatctgc caccagccag ctatcaactc gcgccctggg
840

agggattttt gaagcaactc atcgattgat ttacggcgct aaggatgact ctggtcagag
900

atacctggcc tggtctggac acagtgcccg tgtcggagcc gcgcgagata tggcccgcgc
960

tggagtttca ataccggaga tcatgcaagc tggtggctgg accaatgtaa atattgtcat
1020

gaactatatc cgtaacctgg atagtgaaac aggggcaatg gtgcgcctgc tggaagatgg
1080

cgattagcca ttaacgcgta aatgataagc ttggctgttt tggcggatga gagaagattt
1140

tcagcctgat acagattaaa tcagaacgca ga
1172

<210> 30
<211> 1172

<212> DNA
<213> artificial sequence

<220>
<223> mxoxox2

<400> 30
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caatttactg accgtacacc aaaatttgcc tgcattacct gtcgatgcaa cgagtgatga
120

ggttcgcaag aacctgatgg acatgttcag ggatcgccag gcgttttctg agcatacctg
180

gaaaatgctt ctgtccgttt gccggtcgtg ggcggcatgg tgcaagttga ataaccggaa
240

atggtttccc gcagaacctg aagatgttcg cgattatctt ctatatcttc aggcgcgcgg
300

tctggcagta aaaactatcc agcaacattt gggccagcta aacatgcttc atcgtcggtc
360

cgggctgcca cgaccaagtg acagcaatgc tgtttcactg gttatgcggc ggatccgaaa
420

agaaaacgtt gatgccggtg aacgtgcaaa acaggctcta gcgttcggac gcactgattt
480

cgaccaggtt cgttcactca tggaaaatag cgatcgctgc caggatatac gtaatctggc
540

atttctgggg attgcttata acaccctgtt acgtatagcc gaaattgcca ggatcagggt
600

taaagatatc tcacgtactg acggtgggag aatgttaatc catattggca gaacgaaaac
660

gctggttagc accgcaggtg tagagaaggc acttagcctg ggggtaacta aactggtcga
720

gcgatggatt tccgtctctg gtgtagctga tgatccgaat aactacctgt tttgccgggt
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cagaaaaaat ggtgttgccg cgccatctgc caccggccag ctatcaactc gcgccctggg
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atacctggcc tggtccggac acagtgcccg tgtcggagcc gcgcgagata tggcccgcgc
960

tggagtttca ataccggaga tcatgcaagc tggtggctgg tccaatgtaa atattgtcat
1020

gaactatatc cgtaacctgg atagtgaaac aggggcaatg gtgcgcctgc tggaagatgg
1080

cgattagcca ttaacgcgta aatgataagc ttggctgttt tggcggatga gagaagattt
1140

tcagcctgat acagattaaa tcagaacgca ga
1172

<210> 31
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<212> DNA
<213> artificial sequence

<220>
<223> mxoxox3

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caatttactg accgtacacc aaaatttgcc tgcattaccg atcgatgcaa cgagtgatga
120

ggttcgcaag aacctgatgg acatgttcag ggatcgccag gcgttttctg agcatacctg
180

gaaaatgctt ctgtccgttt gccggtcgtg ggcggcatgg tgcaagttga ataaccggaa
240

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300

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360

cgggctgcca cgaccaagtg acagcaatgc tgtttcactg gttatgcggc ggatccgaaa

420

agaaaacgtt gatgccggtg aacgtgcaaa acaggctcta gcgttcgaac gcactgattt
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cgaccaggtt cgttcactca tggaaaatag cgatcgctgc caggatatac gtaatctggc
540

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taaagatatc tcacgtacta acggtgggag aatgttaatc catattagca gaacgaaaac
660

gctggttagc accgcaggtg tagagaaggc acttagcctg ggggtaacta aactggtcga
720

gcaatggatt tccgtctctg gtgtagctga tgatccgaat aactacctgt tttgccgggt
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cagaaaaaat ggtgttgccg cgccatctgc caccagccgg ctatcaactc gcgccctggg
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agggattttt gaagcaactc atcgattgat ttacggcgct aaggatgact ctggtcagag
900

atacctggcc tggtccggac acagtgcccg tgtcggagcc gcgcgagata tggcccgcgc
960

tggagtttca atactggaga tcatgcaagc tggtggctgg accaatgtaa atattgtcat
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1080

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1172

<210> 32
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<220>

<223> mxoxox4

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120

ggttcgcaag aacctgatgg acatgttcag ggatcgccag gcgttttctg agcatacctg
180

gaaaatgctt ctgtccgttt gccggtcgtg ggcggcatgg tgcaagttga ataaccggaa
240

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tctggcagta aaaactatcc agcaacattt gggccagcta aacatgcttc atcgtcggtc
360

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420

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1080

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1172

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<220>
<223> mxoxox5

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120

ggttcgcaag aacctgatgg ccatgttcag ggatcgccag gcgttttctg agcatacctg
180

gaaaatgctt ctgtccgttt gccggtcgtg ggcggcatgg tgcaagttga ataaccggaa
240

atggtttccc gcagaacctg aagatgttcg cgattatctt ctatatcttc aggcgcgcgg
300

tctggcagta aaaactatcc agcaacattt gggccagcta aacatgcttc atcgtcagtc
360

cgggctgcca cgaccaagtg acagcaatgc tgtttcactg gttatgcggc ggatccgaaa
420

agaaaacgtt gatgccggtg aacgtgcaaa acaggctcta gcgttcgaac gcactgattt
480

cgaccaggtt cgttcactca tggaaaatag cgatcgctgc caggatatac gtaatctggc
540

atttctgggg attgcttata acaccctgtt acgtatagcc gaaattgcca ggatcagggt
600

taaagatatc tcacgtactg acggtgggag aatgttaatc catattggca gaacgaaaac
660

gctggttagc accgcaggtg tagagaaggc acttagcctg ggggtaacta aacaggtcga
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gcgatggatt tccgtctctg gtgtagctga tgatccgaat aactacctgt tttgccgggt
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960

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1080

cgattagcca ttaacgcgta aatgataagc ttggctgttt tggcggatga gagaagattt
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1172

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120

ggttcgcaag aacctgatgg acatgttcag ggatcgccag gcgttttctg agcatacctg
180

gaaaatgctt ctgtccgttt gccggtcgtg ggcggcatgg tgcaagttga ataaccggaa
240

atggtttccc gcagaacctg aagatgttcg cgattatctt ctatatcttc aggcgcgcgg
300

tctggcagta aaaactatcc agcaacattt gggccagcta aacatgcttc atcgtcggtc
360

cgggctgcca cgaccaagtg acagcaatgc tgtttcactg gttatgcggc ggatccgaaa
420

agaaaacgtt gatgccggtg aacgtgcaaa acaggctcta gcgttcgaac gcactgattt
480

cgaccaggtt cgttcactca tggaaaatag cgatcgctgc caggatatac gtaatctggc
540

atttctgggg attgcttata acaccctgtt acgtatagcc gaaattgcca ggatcagggt
600

taaagatatc tcacgtactg acggtgggag aatgttaatc catattggca gaacgaaaac
660

gctggttagc accgcaggtg tagagaaggc acttagcctg ggggtaacta aactggtcga
720

gcgatggatt tccgtctctg gtgtagctga tgatccgaat aactacctgt tttgccgggt
780

cagaaaaaat ggtgttgccg cgccatctgc caccagccag ctatcaactc gcgccctggg
840

agggattttt gaagcaactc atcgattgat ttacggcgct aaggatgact ctggtcagag
900

ataccaggcc tggtctggac acagtgcccg tgtcggagcc gcgcgagata tggcccgcgc
960

tggagtttca ataccggaga tcatgcaagc tggtggctgg tccaatgtaa atattgtcat

1020

gaactatatc cgtaacctgg atagtgaaac aggggcaatg gtgcgcctgc tggaagatgg
1080

cgattagcca ttaacgcgta aatgataagc ttggctgttt tggcggatga gagaagattt
1140

tcagcctgat acagattaaa tcagaacgca ga
1172

<210> 35
<211> 343
<212> PRT
<213> artificial sequence

<220>
<223> mxoxox1

<400> 35

Met Ser Asn Leu Leu Thr Val His Gln Asn Leu Pro Ala Leu Pro Val
1 5 10 15

Asp Ala Thr Ser Asp Glu Val Arg Lys Asn Leu Met Ala Met Phe Arg
20 25 30

Asp Arg Gln Ala Phe Ser Glu His Thr Trp Lys Met Leu Leu Ser Val
35 40 45

Cys Arg Ser Trp Ala Ala Trp Cys Lys Leu Asn Asn Arg Lys Trp Phe
50 55 60

Pro Ala Glu Pro Glu Asp Val Arg Asp Tyr Leu Leu Tyr Leu Gln Ala
65 70 75 80

Arg Gly Leu Ala Val Lys Thr Ile Gln Gln His Leu Gly Gln Leu Asn
85 90 95

Met Leu His Arg Arg Ser Gly Leu Pro Arg Pro Ser Asp Ser Asn Ala
100 105 110

Val Ser Leu Val Met Arg Arg Ile Arg Lys Glu Asn Val Asp Ala Gly
115 120 125

Glu Arg Ala Lys Gln Ala Leu Ala Phe Glu Arg Thr Asp Phe Asp Gln
130 135 140

Val Arg Ser Leu Met Glu Asn Ser Asp Arg Cys Gln Asp Ile Arg Asn
145 150 155 160

Leu Ala Phe Leu Gly Ile Ala Tyr Asn Thr Leu Leu Arg Ile Ala Glu
165 170 175

Ile Ala Arg Ile Arg Val Lys Asp Ile Ser Arg Thr Asn Gly Gly Arg
180 185 190

Met Leu Ile His Ile Gly Arg Thr Lys Thr Leu Val Ser Thr Ala Gly
195 200 205

Val Glu Lys Ala Leu Ser Leu Gly Val Thr Lys Leu Val Glu Arg Trp
210 215 220

Ile Ser Ile Ser Gly Val Ala Asp Asp Pro Asn Asn Tyr Leu Phe Cys
225 230 235 240

Arg Val Arg Lys Asn Gly Val Ala Ala Pro Ser Ala Thr Ser Gln Leu
245 250 255

Ser Thr Arg Ala Leu Gly Gly Ile Phe Glu Ala Thr His Arg Leu Ile
260 265 270

Tyr Gly Ala Lys Asp Asp Ser Gly Gln Arg Tyr Leu Ala Trp Ser Gly
275 280 285

His Ser Ala Arg Val Gly Ala Ala Arg Asp Met Ala Arg Ala Gly Val
290 295 300

```
Ser Ile Pro Glu Ile Met Gln Ala Gly Gly Trp Thr Asn Val Asn Ile
305                 310                 315                 320

Val Met Asn Tyr Ile Arg Asn Leu Asp Ser Glu Thr Gly Ala Met Val
                325                 330                 335

Arg Leu Leu Glu Asp Gly Asp
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<210> 36
<211> 343
<212> PRT
<213> artificial sequence

<220>
<223> mxoxox2

<400> 36

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Met Ser Asn Leu Leu Thr Val His Gln Asn Leu Pro Ala Leu Pro Val
1               5                   10                  15

Asp Ala Thr Ser Asp Glu Val Arg Lys Asn Leu Met Asp Met Phe Arg
            20                  25                  30

Asp Arg Gln Ala Phe Ser Glu His Thr Trp Lys Met Leu Leu Ser Val
        35                  40                  45

Cys Arg Ser Trp Ala Ala Trp Cys Lys Leu Asn Asn Arg Lys Trp Phe
    50                  55                  60

Pro Ala Glu Pro Glu Asp Val Arg Asp Tyr Leu Leu Tyr Leu Gln Ala
65                  70                  75                  80

Arg Gly Leu Ala Val Lys Thr Ile Gln Gln His Leu Gly Gln Leu Asn
                85                  90                  95
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```
Met Leu His Arg Arg Ser Gly Leu Pro Arg Pro Ser Asp Ser Asn Ala
            100                 105                 110

Val Ser Leu Val Met Arg Arg Ile Arg Lys Glu Asn Val Asp Ala Gly
        115                 120                 125

Glu Arg Ala Lys Gln Ala Leu Ala Phe Gly Arg Thr Asp Phe Asp Gln
    130                 135                 140

Val Arg Ser Leu Met Glu Asn Ser Asp Arg Cys Gln Asp Ile Arg Asn
145                 150                 155                 160

Leu Ala Phe Leu Gly Ile Ala Tyr Asn Thr Leu Leu Arg Ile Ala Glu
                165                 170                 175

Ile Ala Arg Ile Arg Val Lys Asp Ile Ser Arg Thr Asp Gly Gly Arg
            180                 185                 190

Met Leu Ile His Ile Gly Arg Thr Lys Thr Leu Val Ser Thr Ala Gly
        195                 200                 205

Val Glu Lys Ala Leu Ser Leu Gly Val Thr Lys Leu Val Glu Arg Trp
    210                 215                 220

Ile Ser Val Ser Gly Val Ala Asp Asp Pro Asn Asn Tyr Leu Phe Cys
225                 230                 235                 240

Arg Val Arg Lys Asn Gly Val Ala Ala Pro Ser Ala Thr Gly Gln Leu
                245                 250                 255

Ser Thr Arg Ala Leu Gly Gly Ile Phe Glu Ala Thr His Arg Leu Ile
            260                 265                 270

Tyr Gly Ala Lys Asp Asp Ser Gly Gln Arg Tyr Leu Ala Trp Ser Gly
        275                 280                 285
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His Ser Ala Arg Val Gly Ala Ala Arg Asp Met Ala Arg Ala Gly Val
290 295 300

Ser Ile Pro Glu Ile Met Gln Ala Gly Gly Trp Thr Asn Val Asn Ile
305 310 315 320

Val Met Asn Tyr Ile Arg Asn Leu Asp Ser Glu Thr Gly Ala Met Val
325 330 335

Arg Leu Leu Glu Asp Gly Asp
340

<210> 37
<211> 343
<212> PRT
<213> artificial sequence

<220>
<223> mxoxox3

<400> 37

Met Ser Asn Leu Leu Thr Val His Gln Asn Leu Pro Ala Leu Pro Ile
1 5 10 15

Asp Ala Thr Ser Asp Glu Val Arg Lys Asn Leu Met Asp Met Phe Arg
20 25 30

Asp Arg Gln Ala Phe Ser Glu His Thr Trp Lys Met Leu Leu Ser Val
35 40 45

Cys Arg Ser Trp Ala Ala Trp Cys Lys Leu Asn Asn Arg Lys Trp Phe
50 55 60

Pro Ala Glu Pro Glu Asp Val Arg Asp Tyr Leu Leu Tyr Leu Gln Ala
65 70 75 80

Arg Gly Leu Ala Val Lys Thr Ile Gln Gln His Leu Gly Gln Leu Asn
85 90 95

```
Met Leu His Arg Arg Ser Gly Leu Pro Arg Pro Ser Asp Ser Asn Ala
            100                 105                 110

Val Ser Leu Val Met Arg Arg Ile Arg Lys Glu Asn Val Asp Ala Gly
        115                 120                 125

Glu Arg Ala Lys Gln Ala Leu Ala Phe Glu Arg Thr Asp Phe Asp Gln
    130                 135                 140

Val Arg Ser Leu Met Glu Asn Ser Asp Arg Cys Gln Asp Ile Arg Asn
145                 150                 155                 160

Leu Ala Phe Leu Gly Ile Ala Tyr Asn Thr Leu Leu Arg Ile Ala Glu
                165                 170                 175

Ile Ala Arg Ile Arg Val Lys Asp Ile Ser Arg Thr Asn Gly Gly Arg
            180                 185                 190

Met Leu Ile His Ile Ser Arg Thr Lys Thr Leu Val Ser Thr Ala Gly
        195                 200                 205

Val Glu Lys Ala Leu Ser Leu Gly Val Thr Lys Leu Val Glu Gln Trp
    210                 215                 220

Ile Ser Val Ser Gly Val Ala Asp Asp Pro Asn Asn Tyr Leu Phe Cys
225                 230                 235                 240

Arg Val Arg Lys Asn Gly Val Ala Ala Pro Ser Ala Thr Ser Arg Leu
                245                 250                 255

Ser Thr Arg Ala Leu Gly Gly Ile Phe Glu Ala Thr His Arg Leu Ile
            260                 265                 270

Tyr Gly Ala Lys Asp Asp Ser Gly Gln Arg Tyr Leu Ala Trp Ser Gly
        275                 280                 285
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His Ser Ala Arg Val Gly Ala Ala Arg Asp Met Ala Arg Ala Gly Val
290 295 300

Ser Ile Leu Glu Ile Met Gln Ala Gly Gly Trp Thr Asn Val Asn Ile
305 310 315 320

Val Met Asn Tyr Ile Arg Asn Leu Asp Ser Glu Thr Gly Ala Met Val
325 330 335

Arg Leu Leu Glu Asp Gly Asp
340

<210> 38
<211> 343
<212> PRT
<213> artificial sequence

<220>
<223> mxoxox4

<400> 38

Met Ser Asn Leu Leu Thr Val His Gln Asn Leu Pro Ala Leu Pro Val
1 5 10 15

Asp Ala Thr Ser Asp Glu Val Arg Lys Asn Leu Met Asp Met Phe Arg
20 25 30

Asp Arg Gln Ala Phe Ser Glu His Thr Trp Lys Met Leu Leu Ser Val
35 40 45

Cys Arg Ser Trp Ala Ala Trp Cys Lys Leu Asn Asn Arg Lys Trp Phe
50 55 60

Pro Ala Glu Pro Glu Asp Val Arg Asp Tyr Leu Leu Cys Leu Gln Ala
65 70 75 80

Arg Gly Leu Ala Val Lys Thr Ile Gln Gln His Leu Gly Gln Leu Asn
85 90 95

Met Leu His Arg Arg Ser Gly Leu Pro Arg Pro Ser Asp Ser Asn Ala
100 105 110

Val Ser Leu Val Met Arg Arg Ile Arg Lys Glu Asn Val Asp Ala Gly
115 120 125

Glu Arg Ala Lys Gln Ala Leu Ala Phe Lys Arg Thr Asp Phe Asp Gln
130 135 140

Val Arg Ser Leu Met Glu Asn Ser Asp Arg Cys Gln Asp Ile Arg Asn
145 150 155 160

Leu Ala Phe Leu Gly Ile Ala Tyr Asn Thr Leu Leu Arg Ile Ala Glu
165 170 175

Ile Ala Arg Ile Arg Val Lys Asp Ile Ser Arg Thr Asp Gly Gly Arg
180 185 190

Met Leu Ile His Ile Gly Arg Thr Lys Thr Leu Val Ser Thr Ala Gly
195 200 205

Val Glu Lys Ala Leu Ser Leu Gly Val Thr Lys Leu Val Glu Arg Trp
210 215 220

Ile Ser Val Ser Gly Val Ala Asp Asp Pro Asn Asn Tyr Leu Phe Cys
225 230 235 240

Arg Val Arg Lys Asn Gly Val Ala Ala Pro Ser Ala Thr Ser Gln Leu
245 250 255

Ser Thr Arg Ala Leu Glu Gly Ile Phe Glu Ala Thr His Arg Leu Ile
260 265 270

Tyr Gly Ala Lys Asp Asp Ser Gly Gln Arg Tyr Gln Ala Trp Ser Gly
275 280 285

His Ser Ala Arg Val Gly Ala Ala Arg Asp Met Ala Arg Ala Gly Val
290 295 300

Ser Ile Pro Glu Ile Met Gln Ala Gly Gly Trp Thr Asn Val Asn Ile
305 310 315 320

Val Met Asn Tyr Ile Arg Asn Leu Asp Ser Glu Thr Gly Ala Met Val
325 330 335

Arg Leu Leu Glu Asp Gly Asp
340

<210> 39
<211> 343
<212> PRT
<213> artificial sequence

<220>
<223> mxoxox5

<400> 39

Met Ser Asn Leu Leu Thr Val His Gln Asn Leu Pro Ala Leu Pro Val
1 5 10 15

Asp Ala Thr Ser Asp Glu Val Arg Lys Asn Leu Met Ala Met Phe Arg
20 25 30

Asp Arg Gln Ala Phe Ser Glu His Thr Trp Lys Met Leu Leu Ser Val
35 40 45

Cys Arg Ser Trp Ala Ala Trp Cys Lys Leu Asn Asn Arg Lys Trp Phe
50 55 60

Pro Ala Glu Pro Glu Asp Val Arg Asp Tyr Leu Leu Tyr Leu Gln Ala
65 70 75 80

Arg Gly Leu Ala Val Lys Thr Ile Gln Gln His Leu Gly Gln Leu Asn
85 90 95

Met Leu His Arg Gln Ser Gly Leu Pro Arg Pro Ser Asp Ser Asn Ala
100 105 110

Val Ser Leu Val Met Arg Arg Ile Arg Lys Glu Asn Val Asp Ala Gly
115 120 125

Glu Arg Ala Lys Gln Ala Leu Ala Phe Glu Arg Thr Asp Phe Asp Gln
130 135 140

Val Arg Ser Leu Met Glu Asn Ser Asp Arg Cys Gln Asp Ile Arg Asn
145 150 155 160

Leu Ala Phe Leu Gly Ile Ala Tyr Asn Thr Leu Leu Arg Ile Ala Glu
165 170 175

Ile Ala Arg Ile Arg Val Lys Asp Ile Ser Arg Thr Asp Gly Gly Arg
180 185 190

Met Leu Ile His Ile Gly Arg Thr Lys Thr Leu Val Ser Thr Ala Gly
195 200 205

Val Glu Lys Ala Leu Ser Leu Gly Val Thr Lys Gln Val Glu Arg Trp
210 215 220

Ile Ser Val Ser Gly Val Ala Asp Asp Pro Asn Asn Tyr Leu Phe Cys
225 230 235 240

Arg Val Arg Lys Asn Gly Val Ala Ala Pro Ser Ala Thr Ser Gln Leu
245 250 255

Ser Thr Arg Ala Leu Gly Gly Ile Phe Glu Ala Thr His Arg Leu Ile
260 265 270

Tyr Gly Ala Lys Asp Asp Ser Gly Gln Arg Tyr Leu Ala Trp Ser Gly
275 280 285

His Ser Ala Arg Val Gly Ala Ala Arg Asp Met Ala Arg Ala Gly Val
290 295 300

Ser Ile Pro Glu Ile Met Gln Ala Gly Gly Trp Ser Asn Val Asn Ile
305 310 315 320

Val Met Asn Tyr Ile Arg Asn Leu Asp Ser Glu Thr Gly Ala Met Val
325 330 335

Arg Leu Leu Glu Asp Gly Asp
340

<210> 40
<211> 343
<212> PRT
<213> artificial sequence

<220>
<223> mxoxox6

<400> 40

Met Ser Asn Leu Leu Thr Val His Gln Asn Leu Pro Ala Leu Pro Val
1 5 10 15

Asp Ala Thr Ser Asp Glu Val Arg Lys Asn Leu Met Asp Met Phe Arg
20 25 30

Asp Arg Gln Ala Phe Ser Glu His Thr Trp Lys Met Leu Leu Ser Val
35 40 45

Cys Arg Ser Trp Ala Ala Trp Cys Lys Leu Asn Asn Arg Lys Trp Phe
50 55 60

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Pro Ala Glu Pro Glu Asp Val Arg Asp Tyr Leu Leu Tyr Leu Gln Ala
65                  70                  75                  80

Arg Gly Leu Ala Val Lys Thr Ile Gln Gln His Leu Gly Gln Leu Asn
                85                  90                  95

Met Leu His Arg Arg Ser Gly Leu Pro Arg Pro Ser Asp Ser Asn Ala
            100                 105                 110

Val Ser Leu Val Met Arg Arg Ile Arg Lys Glu Asn Val Asp Ala Gly
        115                 120                 125

Glu Arg Ala Lys Gln Ala Leu Ala Phe Glu Arg Thr Asp Phe Asp Gln
    130                 135                 140

Val Arg Ser Leu Met Glu Asn Ser Asp Arg Cys Gln Asp Ile Arg Asn
145                 150                 155                 160

Leu Ala Phe Leu Gly Ile Ala Tyr Asn Thr Leu Leu Arg Ile Ala Glu
                165                 170                 175

Ile Ala Arg Ile Arg Val Lys Asp Ile Ser Arg Thr Asp Gly Gly Arg
            180                 185                 190

Met Leu Ile His Ile Gly Arg Thr Lys Thr Leu Val Ser Thr Ala Gly
        195                 200                 205

Val Glu Lys Ala Leu Ser Leu Gly Val Thr Lys Leu Val Glu Arg Trp
    210                 215                 220

Ile Ser Val Ser Gly Val Ala Asp Asp Pro Asn Asn Tyr Leu Phe Cys
225                 230                 235                 240

Arg Val Arg Lys Asn Gly Val Ala Ala Pro Ser Ala Thr Ser Gln Leu
                245                 250                 255
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Ser Thr Arg Ala Leu Gly Gly Ile Phe Glu Ala Thr His Arg Leu Ile
260 265 270

Tyr Gly Ala Lys Asp Asp Ser Gly Gln Arg Tyr Gln Ala Trp Ser Gly
275 280 285

His Ser Ala Arg Val Gly Ala Ala Arg Asp Met Ala Arg Ala Gly Val
290 295 300

Ser Ile Pro Glu Ile Met Gln Ala Gly Gly Trp Ser Asn Val Asn Ile
305 310 315 320

Val Met Asn Tyr Ile Arg Asn Leu Asp Ser Glu Thr Gly Ala Met Val
325 330 335

Arg Leu Leu Glu Asp Gly Asp
340

<210> 41
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<220>
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<222> (6)..(7)
<223> nn is either TT, TG, GT, GG, TC, CC, or AA

<400> 41
ataacnncgt ata
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<210> 42
<211> 13
<212> DNA
<213> artificial sequence

<220>
<223> loxK2

<400> 42
ataacaacgt ata
13

<210> 43
<211> 13
<212> DNA
<213> artificial sequence

<220>
<223> loxK1

<400> 43
atacctttgt ata
13

<210> 44
<211> 34
<212> DNA
<213> artificial sequence

<220>
<223> loxP

<400> 44
ataacttcgt atataccttt ctatagcaag ttat
34

<210> 45
<211> 34
<212> DNA
<213> artificial sequence

<220>
<223> loxK2

<400> 45
ataacaacgt atataccttt ctatagcttg ttat
34

<210> 46

<211> 34
<212> DNA
<213> artificial sequence

<220>
<223> loxK1

<400> 46
ataccttttgt atataccttt ctatagaaag gtat
34

<210> 47
<211> 34
<212> DNA
<213> artificial sequence

<220>
<223> loxK2 'GG'

<400> 47
ataacggcgt atataccttt ctatagcccg ttat
34

<210> 48
<211> 34
<212> DNA
<213> artificial sequence

<220>
<223> loxK2 'CC'

<400> 48
ataaccccgt atataccttt ctatagcggg ttat
34

<210> 49
<211> 34
<212> DNA
<213> artificial sequence

<220>
<223> loxK2 'TC'

<400> 49
ataactccgt atataccttt ctatagcgag ttat

34

<210> 50
<211> 34
<212> DNA
<213> artificial sequence

<220>
<223> loxK2 'GT'

<400> 50
ataacgtcgt atataccttt ctatagcacg ttat
34

<210> 51
<211> 34
<212> DNA
<213> artificial sequence

<220>
<223> loxK2 'TG'

<400> 51
ataactgcgt atataccttt ctatagccag ttat
34

<210> 52
<211> 34
<212> DNA
<213> artificial sequence

<220>
<223> LoxP

<400> 52
ataacttcgt ataatgtatg ctatacgaag ttat
34

<210> 53
<211> 34
<212> DNA
<213> artificial sequence

<220>

<223> LoxK1

<400> 53
gagcctttgt atataccttt ctatacaaag gctt
34

<210> 54
<211> 34
<212> DNA
<213> artificial sequence

<220>
<223> loxK2

<400> 54
gatacaacgt atataccttt ctatacgttg tatt
34

<210> 55
<211> 64
<212> DNA
<213> artificial sequence

<220>
<223> Gene

<400> 55
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60

gctt
64

<210> 56
<211> 33
<212> DNA
<213> artificial sequence

<220>
<223> oligonucleotide

<400> 56
agcttggagg ctatcatgtc gaccaagcta gca
33

<210> 57
<211> 33
<212> DNA
<213> artificial sequence

<220>
<223> oligonucleotide

<400> 57
gatctgctag cttggtcgac atgatagcct cca
33

<210> 58
<211> 35
<212> DNA
<213> artificial sequence

<220>
<223> oligonucleotide

<400> 58
gatctgatat ctgcggccgc tgacgtgact cgagt
35

<210> 59
<211> 35
<212> DNA
<213> artificial sequence

<220>
<223> oligonucleotide

<400> 59
ctagactcga gtcacgtcag cggccgcaga tatca
35

<210> 60
<211> 13
<212> DNA
<213> artificial sequence

<220>
<223> oligonucleotide

<400> 60
gaagttccta ttc
13

<210> 61
<211> 8
<212> DNA
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<220>
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<400> 61
tctagaaa
8

<210> 62
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<212> DNA
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<220>
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<400> 62
gtataggaac ttc
13

<210> 63
<211> 27
<212> DNA
<213> artificial sequence

<220>
<223> oligonucleotide

<400> 63
gaagttccta ttccgaagtt cctattc
27

<210> 64
<211> 6
<212> DNA
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<220>
<223> oligonucleotide

<400> 64
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6

<210> 65
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<220>
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<400> 65
gaagttcata ttc
13

<210> 66
<211> 13
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<220>
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<400> 66
gtatatgaac ttc
13

<210> 67
<211> 13
<212> DNA
<213> artificial sequence

<220>
<223> oligonucleotide

<400> 67
gaagttacta ttc
13

<210> 68
<211> 13
<212> DNA
<213> artificial sequence

<220>
<223> oligonucleotide

<400> 68
gtatagtaac ttc
13